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OI IO IntelliGenetics
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GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Thu 21 Feb 102 14:55:14-PST

Solution Parameters:

Nucleic Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off

AMINO-Res-length = 2
DEletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

6. aa419064 (1-375)
7. US-09-274-1 (1-1734)

Region Alignment: (listed in Clustered order)

```
aa419064 1 GGGCCATGG CTGGAG CGCCCGCAGACCCCGCGAGCCGCGCTTGT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
US-09-274- 1 ggcacagagcgccggccatgggctcgcagcccgcccgaaaccccgagcccgccctgtg
consensus ggacacagggcgccggccatgggctcgcagcccgcccgaaaccccgagcccgccctgtg

aa419064 46 CTGGGGGTGACTGGAGGCCAGATGGTGCATCATATGGCCAGTCTACTACAAACAGACCAT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
US-09-274- 62 CTGGGGGTGACTGGAGGCCAGATGGTGCATCATATGGCCAGTCTACTACAAACAGACCAT
consensus CTGGGGGTGACTGGAGGCCAGATGGTGCATCATATGGCCAGTCTACTACAAACAGACCAT

aa419064 107 CGGCTTCTTCTATAAACACAGTGGCAAGAGCTCAGCTCCCACTGGCGGCCAAGGATGTG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
US-09-274- 123 CGGCTTCTTCTATAAACACAGTGGCAAGAGCTCAGCTCCCACTGGCGGCCAAGGATGTG
consensus CGGCTTCTTCTATAAACACAGTGGCAAGAGCTCAGCTCCCACTGGCGGCCAAGGATGTG

aa419064 168 GTGCTGGTGGCACTGGGGCTGACCGTCAAGCGTGTGTGTGCTGCTGACCAATCTGCTGGTCA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
US-09-274- 184 GTGCTGGTGGCACTGGGGCTGACCGTCAAGCGTGTGTGTGCTGCTGACCAATCTGCTGGTCA
consensus GTGCTGGTGGCACTGGGGCTGACCGTCAAGCGTGTGTGTGCTGCTGACCAATCTGCTGGTCA

aa419064 229 TAGCAGCCATCGCTCCAAACCGCGCTTCCACAGCCCATCTACTACCTGCTCGGCAATCT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
US-09-274- 245 TAGCAGCCATCGCTCCAAACCGCGCTTCCACAGCCCATCTACTACCTGCTCGGCAATCT
consensus TAGCAGCCATCGCTCCAAACCGCGCTTCCACAGCCCATCTACTACCTGCTCGGCAATCT

aa419064 290 GGCCGGGTGACCTCTTCGCGGGCGTGGC TACCTCTTCTCATGTTCACACTGCTGCC
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
US-09-274- 306 GGCCGGGTGACCTCTTCGCGGGCGTGGC TACCTCTTCTCATGTTCACACTGCTGCC
consensus GGCCGGGTGACCTCTTCGCGGGCGTGGC TACCTCTTCTCATGTTCACACTGCTGCC
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Multiple Sequence Alignment Program
Case 5.4

Thu 21 Feb 102 14:54:03-EST

Solution Parameters:

- Amino Alphabet = Identity
- Output line length = 80
- Compress = Off
- Histogram = Off
- Randomization = Off
- AMINO-Res-length = 2
- Deletion-weight = 5.00
- Length-factor = 0
- Matching-weight = 1.00
- CLEIC-Res-length = 4
- read-factor = 50

Clustered order of selected sequences:

1. HARRIS-EDG4.PEP (1-382)
2. US-09-274-752D-1 (1-382)

Region Alignment: (listed in Clustered order)

HARRIS-EDG 1 MVIMGQCYNETIGFFYNNSGKELSSHWRPKDVVVALGLTVSVLVLLTNLLVIAAIAASNR
US-09-274- 1 MVIMGQCYNETIGFFYNNSGKELSSHWRPKDVVVALGLTVSVLVLLTNLLVIAAIAASNR
consensus MVIMGQCYNETIGFFYNNSGKELSSHWRPKDVVVALGLTVSVLVLLTNLLVIAAIAASNR
HARRIS-EDG 62 RFHOPYYLLGNLAADLFAGVAYLFLMFHTGPTARLSLEGWFLRQGLDTSLTASVATL
US-09-274- 62 RFHOPYYLLGNLAADLFAGVAYLFLMFHTGPTARLSLEGWFLRQGLDTSLTASVATL
consensus RFHOPYYLLGNLAADLFAGVAYLFLMFHTGPTARLSLEGWFLRQGLDTSLTASVATL
HARRIS-EDG 123 LAIAVERHRSVMVOLHSRLPRGRVVMILIVGVWVAALGLGLLPAHSHWHCLCALDRCRMAP
US-09-274- 123 LAIAVERHRSVMVOLHSRLPRGRVVMILIVGVWVAALGLGLLPAHSHWHCLCALDRCRMAP
consensus LAIAVERHRSVMVOLHSRLPRGRVVMILIVGVWVAALGLGLLPAHSHWHCLCALDRCRMAP
HARRIS-EDG 184 LLSRSYLAVWALSLLVFLLMVAVYTRIFFYVRRRVQSMAEHVSCHPRYRETTLSLVKTIV
US-09-274- 184 LLSRSYLAVWALSLLVFLLMVAVYTRIFFYVRRRVQSMAEHVSCHPRYRETTLSLVKTIV
consensus LLSRSYLAVWALSLLVFLLMVAVYTRIFFYVRRRVQSMAEHVSCHPRYRETTLSLVKTIV
HARRIS-EDG 245 IILGAFVVCWTPGGQVLLLDGLGCESCNCVLAVERKYLFLLAELAEANSLVNAAVYSCRDsEMRRT
US-09-274- 245 IILGAFVVCWTPGGQVLLLDGLGCESCNCVLAVERKYLFLLAELAEANSLVNAAVYSCRDsEMRRT
consensus IILGAFVVCWTPGGQVLLLDGLGCESCNCVLAVERKYLFLLAELAEANSLVNAAVYSCRD-EMRRT
HARRIS-EDG 306 FRLLCCACLRQSTRESVHYTSSAOGGASTRIMLPENGHPMLTPPFYSYLELQRYAASNKST
US-09-274- 306 FRLLCCACLRQSTRESVHYTSSAOGGASTRIMLPENGHPMLTPPFYSYLELQRYAASNKST
consensus FRLLCCACLRQSTRESVHYTSSAOGGASTRIMLPENGHPMLTPPFYSYLELQRYAASNKST

HARRIS-EDG 367 APDDLWVLLAQPNOOD
US-09-274- 367 APDDLWVLLAQPNOOD
consensus APDDLWVLLAQPNOOD

Alignment score = 380.00

Scoring matrix:

	1	2
1	380	
2		